AMENDMENTS TO THE CLAIMS

1. **(Currently amended)** A screening and/or quantification method of one or more transcriptional factors(s) present in a cell or cell lysate, said method comprising the steps of:

a. binding to an insoluble solid support double-stranded DNA sequence(s) at the concentration of at least 0.01 pmole/cm^2 of said solid support surface, wherein the solid support is an array bearing at least 4 spots/cm^2 of solid support surface, each spot containing double-stranded DNA sequence(s) for the binding of transcriptional factor(s), said double-stranded DNA sequence comprising a specific sequence, said specific sequence being able to bind said one or more transcriptional factor(s) and said double-stranded DNA sequence being connected to the surface of the solid support by a spacer corresponding to or comprising at least a double-stranded DNA nucleotide sequence of ~~at least 20~~ between about 50 and about 250 base pairs;

b. putting into contact said one or more transcriptional factor(s) with said bound double-stranded DNA sequence(s); and

c. identifying and/or quantifying a signal resulting from the binding of said transcriptional factor(s) upon said double-stranded DNA sequence(s).

2. **(Original)** The method according to claim 1, wherein the transcriptional factor is present in solution at concentration lower than 20 nmolar (nM).

3. **(Previously presented)** The method according to claim 1, wherein the specific sequence of the double-stranded DNA sequence(s) able to bind with the transcriptional factor(s) is located at a distance of at least about 6.8 nm from the surface of the solid support.

4. **(Original)** The method according to claim 1, wherein the signal resulting from the binding of the transcriptional factor upon the double-stranded DNA sequence is a non-radioactive resulting signal.

5. **(Previously presented)** The method according to claim 1, wherein the signal resulting from the binding of the transcriptional factor upon the double-stranded DNA sequence is obtained through an enzymatic reaction.

6. **(Previously presented)** The method according to claim 1, for the screening and/or quantification of multiple different transcriptional factors present in a same biological sample.

7. **(Previously presented)** The method according to claim 1, for the screening and/or quantification of transcriptional factors selected from the group consisting of NF-KB, AP-1, CREB, SP-1, C/EBP, GR, HIF-1, Myc, NF-AT, Oct, TBP, CBF-1 and factors listed in table 1.

8. **(Previously presented)** The method according to claim 1, for the screening and/or quantification of multiple different transcriptional factors upon a same support upon the same multiwell plate.

9. **(Cancelled)**

10. **(Previously presented)** The method according to claim 1, wherein the spacer between the double-stranded DNA sequence(s) and the solid support is at least about 13.5 nm.

11. **Cancelled**

12. **(Previously presented)** The method according to claim 1, wherein the binding of the double-stranded DNA sequence(s) to the insoluble solid support is of non-covalent type and includes a binding pair comprising a first member and a second member, said first member being bound to the double-stranded DNA sequence, said second member being bound to the surface of the solid support.

13. **(Original)** The method according to claim 1, wherein the double-stranded DNA sequence(s) are covalently bound to the surface of the insoluble solid support.

14. **(Original)** The method according to claim 1, wherein the consensus sequence is repeated on the same molecule.

15. **(Original)** The method according to claim 1, wherein the double-stranded DNA sequences fixed on the support surface contain in part or totally one or several of the consensus DNA sequences presented in the table 1.

16. **(Original)** The method according to claim 1, wherein said transcriptional factor is the HIV integrase.

17. **(Original)** The method according to claim 1, comprising the step of identification of at least one characteristic specific of the transcriptional factor activation.

18. **(Original)** The method according to claim 1, which comprises the steps of screening, quantifying and/or recovering compounds able to bind to said transcriptional factor(s) or inhibit the binding of transcriptional factor(s) to the specific sequence upon the double-stranded DNA sequence(s) bound to said solid support.

19. **(Original)** The method according to claim 1, which comprises the steps of screening, quantifying and/or recovering compounds which modulate the binding and/or the activity of the said transcriptional factor(s) when they are put in contact with cells, tissues or organisms.

20. **(Original)** The method according to claim 1, which comprises the steps of screening, quantifying and/or recovering compounds which modulate the activity of enzyme(s) or protein(s) acting on transcriptional factor(s) and then assayed for the binding to and/or activity of said transcriptional factor(s).

21. **(Original)** A method according to claim 1, which comprises the step of identification of transcriptional factor(s) and/or of peptides which are part of their active complex.

22. **(Original)** The method according to claim 1, which comprises the step of adding in the cell lysate an externally added transcriptional factor or a compound which is able to bind to the consensus sequence.

23. **(Withdrawn)** A screening, diagnostic and/or quantification kit comprising reagents and media for performing the method according to claim 1.

24. **(Withdrawn)** The kit according to claim 23 for the screening and/or quantification of a transcriptional factor(s) or a compound able to bind to said transcriptional factor(s) or inhibit the binding of said transcriptional factor(s) to a specific nucleotide sequence, which comprises double-stranded DNA sequence(s) bound to an insoluble solid support at a concentration of at least about 0.01 pmole/cm^2 of solid support surface.

25. **(Withdrawn)** The kit according to claim 23, comprising a solid support bearing on its surface one or several double stranded DNA consensus sequences at a concentration of at least 0.01 pmole/cm^2 comprising in part or totally one or several of the consensus sequence(s) listed in table 1 allowing the binding of transcriptional factor(s) present in solution and their detection and/or quantification.

26. **(Withdrawn)** The kit according to claim 23, wherein the solid support is an array having at least 4 spot/cm^2 of solid support surface containing double-stranded DNA sequence(s) for the binding of the transcriptional factor(s).

27. **(Withdrawn)** The kit according to claim 23, wherein the double-stranded DNA sequence(s) comprises between the specific sequence able to bind the transcriptional factor(s) and the surface of the solid support, a spacer of at least about 13.5 nm.

28. **(Withdrawn)** The kit according to claim 23, wherein said spacer is a double-stranded DNA nucleotide sequence of at least 20 base pairs.

29. **(Withdrawn)** The kit according to the claim 27, wherein the spacer is a double-stranded DNA nucleotide sequence of at least 40 base pairs.

30. **(Withdrawn)** The kit according to claim 23, wherein the double-stranded DNA sequence(s) are bound to a first member of a binding pair (preferably biotin), able to interact with a second member of the binding pair (preferably streptavidin) bound to the surface of the solid support.

31. **(Withdrawn)** The kit according to claim 23, wherein the double-stranded DNA sequence(s) are covalently bound to the surface of the solid support.

32. **(Withdrawn)** The compounds identified and/or recovered by the method according to claim 19.

33. **(Withdrawn)** Pharmaceutical composition comprising an adequate pharmaceutical carrier and the unknown compound according to claim 32.

34. **(Previously presented)** The method of Claim 36, wherein said binding pair is biotin/streptavidin.

35. **Cancelled**

36. **(Previously presented)** The method according to claim 12, wherein the binding pair is selected from the group consisting of biotin/streptavidin, hapten/receptor and antigen/antibody binding pair.

37. **(Previously presented)** The method according to claim 1, wherein step b) comprises putting into contact said one or more transcriptional factor(s) in a cell lysate with said bound double-stranded DNA sequence(s).

38. **(Previously presented)** The method according to claim 1, wherein said spacer is a double-stranded DNA nucleotide sequence of at least 40 base pairs.